



Supplementary Figure 5. Gene expression and pathway enrichment analysis of CD8⁺ T cell clusters. **A**, Heatmap showing differentially expressed genes between memory-like *KLF2*⁺ and exhausted-like *MKI67*⁺ CD8⁺ T-cells. Gene signature scores related to cell cycle and clinical response are indicated on the top bars. **B**, Top downregulated GO biological processes in *EGR2* compared to *AAVS1* knockout CAR T-cells.